

A. Gupta

#10

1653

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/163,648

DATE: 05/15/2000

TIME: 12:05:29

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\05152000\I163648.raw

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3 <110> APPLICANT: Acton, Susan L. et al.
5 <120> TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
6 DIAGNOSTIC USES THEREFOR
8 <130> FILE REFERENCE: MNI-132CP
10 <140> CURRENT APPLICATION NUMBER: 09/163,648
11 <141> CURRENT FILING DATE: 1998-09-30
13 <150> PRIOR APPLICATION NUMBER: 08/989,299
14 <151> PRIOR FILING DATE: 1997-12-11
16 <160> NUMBER OF SEQ ID NOS: 24
18 <170> SOFTWARE: PatentIn Ver. 2.0
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21 <211> LENGTH: 3396
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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26 <221> NAME/KEY: CDS
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32 tatcttggtt cacaggggac g atg tca agc tct tcc tgg ctg ctt ctg agc 111
33 Met Ser Ser Ser Ser Trp Leu Leu Leu Ser
34 1 5 10
36 ctt gtt gct gta act gct gct cag tcc acc att gag gaa cag gcc aag 159
37 Leu Val Ala Val Thr Ala Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys
38 15 20 25
40 aca ttt ttg gac aag ttt aac cac gaa gcc gaa gac ctg ttc tat caa 207
41 Thr Phe Leu Asp Lys Phe Asn His Glu Ala Glu Asp Leu Phe Tyr Gln
42 30 35 40
44 agt tca ctt gct tct tgg aat tat aac acc aat att act gaa gag aat 255
45 Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn
46 45 50 55
48 gtc caa aac atg aat aat gct ggg gac aaa tgg tct gcc ttt tta aag 303
49 Val Gln Asn Met Asn Asn Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys
50 60 65 70
52 gaa cag tcc aca ctt gcc caa atg tat cca cta caa gaa att cag aat 351
53 Glu Gln Ser Thr Leu Ala Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn
54 75 80 85 90
56 ctg aca gtc aag ctt cag ctg cag gct ctt cag caa aat ggg tct tca 399
57 Leu Thr Val Lys Leu Gln Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser
58 95 100 105
60 gtg ctg tca gaa gac aag agc aaa cgg ttg aac aca att cta aat aca 447
61 Val Leu Ser Glu Asp Lys Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr
62 110 115 120
64 atg agc acc atc tac agt act gga aaa gtt tgt aac cca gat aat cca 495
65 Met Ser Thr Ile Tyr Ser Thr Gly Lys Val Cys Asn Pro Asp Asn Pro
66 125 130 135
68 caa gaa tgc tta tta ctt gaa cca ggt ttg aat gaa ata atg gca aac 549

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72 agt tta gac tac aat gag agg ctc tgg gct tgg gaa agc tgg aga tct 591
73 Ser Leu Asp Tyr Asn Glu Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser
74 155      160      165      170
76 gag gtc ggc aag cag ctg agg cca tta tat gaa gag tat gtg gtc ttg 639
77 Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu
78      175      180      185
80 aaa aat gag atg gca aga gca aat cat tat gag gac tat ggg gat tat 687
81 Lys Asn Glu Met Ala Arg Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr
82      190      195      200
84 tgg aga gga gac tat gaa gta aat ggg gta gat ggc tat gac tac agc 735
85 Trp Arg Gly Asp Tyr Glu Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser
86      205      210      215
88 cgc ggc cag ttg att gaa gat gtg gaa cat acc ttt gaa gag att aaa 783
89 Arg Gly Gln Leu Ile Glu Asp Val Glu His Thr Phe Glu Glu Ile Lys
90      220      225      230
92 cca tta tat gaa cat ctt cat gcc tat gtg agg gca aag ttg atg aat 831
93 Pro Leu Tyr Glu His Leu His Ala Tyr Val Arg Ala Lys Leu Met Asn
94 235      240      245      250
96 gcc tat cct tcc tat atc agt cca att gga tgc ctc cct gct cat ttg 879
97 Ala Tyr Pro Ser Tyr Ile Ser Pro Ile Gly Cys Leu Pro Ala His Leu
98      255      260      265
100 ctt ggt gat atg tgg ggt aga ttt tgg aca aat ctg tac tct ttg aca 927
101 Leu Gly Asp Met Trp Gly Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr
102      270      275      280
104 gtt ccc ttt gga cag aaa cca aac ata gat gtt act gat gca atg gtg 975
105 Val Pro Phe Gly Gln Lys Pro Asn Ile Asp Val Thr Asp Ala Met Val
106      285      290      295
108 gac cag gcc tgg gat gca cag aga ata ttc aag gag gcc gag aag ttc 1023
109 Asp Gln Ala Trp Asp Ala Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe
110      300      305      310
112 ttt gta tct gtt ggt ctt cct aat atg act caa gga ttc tgg gaa aat 1071
113 Phe Val Ser Val Gly Leu Pro Asn Met Thr Gln Gly Phe Trp Glu Asn
114 315      320      325      330
116 tcc atg cta acg gac cca gga aat gtt cag aaa gca gtc tgc cat ccc 1119
117 Ser Met Leu Thr Asp Pro Gly Asn Val Gln Lys Ala Val Cys His Pro
118      335      340      345
120 aca gct tgg gac ctg ggg aag ggc gac ttc agg atc ctt atg tgc aca 1167
121 Thr Ala Trp Asp Leu Gly Lys Gly Asp Phe Arg Ile Leu Met Cys Thr
122      350      355      360
124 aag gtg aca atg gac gac ttc ctg aca gct cat gat gag atg ggg cat 1215
125 Lys Val Thr Met Asp Asp Phe Leu Thr Ala His His Glu Met Gly His
126      365      370      375
128 atc cag tat gat atg gca tat gct gca caa cct ttt ctg cta aga aat 1263
129 Ile Gln Tyr Asp Met Ala Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn
130      380      385      390
132 gga gct aat gaa gga ttc cat gaa gct gtt ggg gaa atc atg tca ctt 1311
133 Gly Ala Asn Glu Gly Phe His Glu Ala Val Gly Glu Ile Met Ser Leu

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134 395          400          405          410
136 tct gca gcc aca cct aag cat tta aaa tcc att ggt ctt ctg tca ccc 1359
137 Ser Ala Ala Thr Pro Lys His Leu Lys Ser Ile Gly Leu Leu Ser Pro
138          415          420          425
140 gat ttt caa gaa gac aat gaa aca gaa ata aac ttc ctg ctc aaa caa 1407
141 Asp Phe Gln Glu Asp Asn Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln
142          430          435          440
144 gca ctc acg att gtt ggg act ctg cca ttt act tac atg tta gag aag 1455
145 Ala Leu Thr Ile Val Gly Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys
146          445          450          455
148 tgg agg tgg atg gtc ttt aaa ggg gaa att ccc aaa gac cag tgg atg 1503
149 Trp Arg Trp Met Val Phe Lys Gly Glu Ile Pro Lys Asp Gln Trp Met
150          460          465          470
152 aaa aag tgg tgg gag atg aag cga gag ata gtt ggg gtg gtg gaa cct 1551
153 Lys Lys Trp Trp Glu Met Lys Arg Glu Ile Val Gly Val Val Glu Pro
154 475          480          485          490
156 gtg ccc cat gat gaa aca tac tgt gac ccc gca tct ctg ttc cat gtt 1599
157 Val Pro His Asp Glu Thr Tyr Cys Asp Pro Ala Ser Leu Phe His Val
158          495          500          505
160 tct aat gat tac tca ttc att cga tat tac aca agg acc ctt tac caa 1647
161 Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Thr Arg Thr Leu Tyr Gln
162          510          515          520
164 ttc cag ttt caa gaa gca ctt tgt caa gca gct aaa cat gaa ggc cct 1695
165 Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala Ala Lys His Glu Gly Pro
166          525          530          535
168 ctg cac aaa tgt gac atc tca aac tct aca gaa gct gga cag aaa ctg 1743
169 Leu His Lys Cys Asp Ile Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu
170          540          545          550
172 ttc aat atg ctg agg ctt gga aaa tca gaa ccc tgg acc cta gca ttg 1791
173 Phe Asn Met Leu Arg Leu Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu
174 555          560          565          570
176 gaa aat gtt gta gga gca aag aac atg aat gta agg cca ctg ctc aac 1839
177 Glu Asn Val Val Gly Ala Lys Asn Met Asn Val Arg Pro Leu Leu Asn
178          575          580          585
180 tac ttt gag ccc tta ttt acc tgg ctg aaa gac cag aac aag aat tct 1887
181 Tyr Phe Glu Pro Leu Phe Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser
182          590          595          600
184 ttt gtg gga tgg agt acc gac tgg agt cca tat gca gac caa agc atc 1935
185 Phe Val Gly Trp Ser Thr Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile
186          605          610          615
188 aaa gtg agg ata agc cta aaa tca gct ctt gga gat aaa gca tat gaa 1983
189 Lys Val Arg Ile Ser Leu Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu
190          620          625          630
192 tgg aac gac aat gaa atg tac ctg ttc cga tca tct gtt gca tat gct 2031
193 Trp Asn Asp Asn Glu Met Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala
194 635          640          645          650
196 atg agg cag tac ttt tta aaa gta aaa aat cag atg att ctt ttt ggg 2079
197 Met Arg Gln Tyr Phe Leu Lys Val Lys Asn Gln Met Ile Leu Phe Gly
198          655          660          665

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202          670          675          680
204 ttc ttt gtc act gca cct aaa aat gtg tct gat atc att cct aga act 2175
205 Phe Phe Val Thr Ala Pro Lys Asn Val Ser Asp Ile Ile Pro Arg Thr
206          685          690          695
208 gaa gtt gaa aag gcc atc agg atg tcc cgg agc cgt atc aat gat gct 2223
209 Glu Val Glu Lys Ala Ile Arg Met Ser Arg Ser Arg Ile Asn Asp Ala
210          700          705          710
212 ttc cgt ctg aat gac aac agc cta gag ttt ctg ggg ata cag cca aca 2271
213 Phe Arg Leu Asn Asp Asn Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr
214 715          720          725          730
216 ctt gga cct cct aac cag ccc cct gtt tcc ata tgg ctg att gtt ttt 2319
217 Leu Gly Pro Pro Asn Gln Pro Pro Val Ser Ile Trp Leu Ile Val Phe
218          735          740          745
220 gga gtt gtg atg gga gtg ata gtg gtt ggc att gtc atc ctg atc ttc 2367
221 Gly Val Val Met Gly Val Ile Val Val Gly Ile Val Ile Leu Ile Phe
222          750          755          760
224 act ggg atc aga gat cgg aag aag aaa aat aaa gca aga agt gga gaa 2415
225 Thr Gly Ile Arg Asp Arg Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu
226          765          770          775
228 aat cct tat gcc tcc atc gat att agc aaa gga gaa aat aat cca gga 2463
229 Asn Pro Tyr Ala Ser Ile Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly
230          780          785          790
232 ttc caa aac act gat gat gtt cag acc tcc ttt tagaaaaatc tatgtttttc 2516
233 Phe Gln Asn Thr Asp Asp Val Gln Thr Ser Phe
234 795          800          805
236 ctcttgaggt gattttgttg tatgtaaatg ttaatttcac ggtatagaaa atataagatg 2576
238 ataaagatat cattaaatgt caaaactatg actctgttca gaaaaaaaat tgtccaaaga 2636
240 caacatggcc aaggagagag catcttcatt gacattgctt tcagtatatta tttctgtctc 2696
242 tggatttgac ttctgttctg ttctttaata aggattttgt attagagtat attagggaaa 2756
244 gtgtgtattt ggtctcacag gctgttcagg gataatctaa atgtaaatgt ctgttgattt 2816
246 tctgaagttg aaaacaagga tatatcattg gagcaagtgt tggatcttgt atggaatatg 2876
248 gatggatcac ttgtaaggac agtgcctggg aactggtgta gctgcaagga ttgagaatgg 2936
250 catgcattag ctcactttca tttaatccat tgtcaaggat gacatgcttt ctccacagta 2996
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254 ttcaaggtga cagggtctaaa gagagaagaa tccaggggaa aggtagagga cattgctttt 3116
256 tcaacttcaa ggtgcttgat caacatctcc ctgacaacac aaaactagag ccagggggcct 3176
258 ccgtgaaact ccagagcatg cctgatagaa actcatttct actgtttctt aactgtggag 3236
260 tgaatggaaa ttccaactgt atgttcaccc tctgaagtgg gtacccagtc tcttaaatct 3296
262 tttgtatttg ctacagtggt ttgagcagtg ctgagcacia agcagacact caataaatgc 3356
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269 <212> TYPE: PRT
270 <213> ORGANISM: Homo sapiens
272 <400> SEQUENCE: 2
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276 Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe
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279 Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp
280      35      40      45
282 Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn
283      50      55      60
285 Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala
286      65      70      75      80
288 Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln
289      85      90      95
291 Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys
292      100     105     110
294 Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser
295      115     120     125
297 Thr Gly Lys Val Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu
298      130     135     140
300 Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu
301 145      150     155     160
303 Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu
304      165     170     175
306 Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg
307      180     185     190
309 Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
310      195     200     205
312 Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu
313      210     215     220
315 Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu
316 225      230     235     240
318 His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile
319      245     250     255
321 Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly
322      260     265     270
324 Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys
325      275     280     285
327 Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala
328      290     295     300
330 Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
331 305      310     315     320
333 Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro
334      325     330     335
336 Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly
337      340     345     350
339 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp
340      355     360     365
342 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
343      370     375     380
345 Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
346 385      390     395     400
348 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys

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